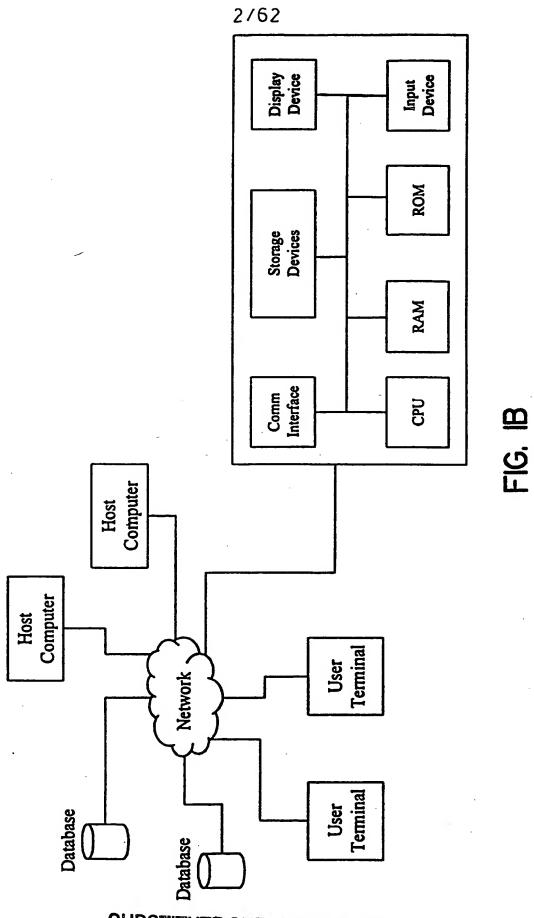
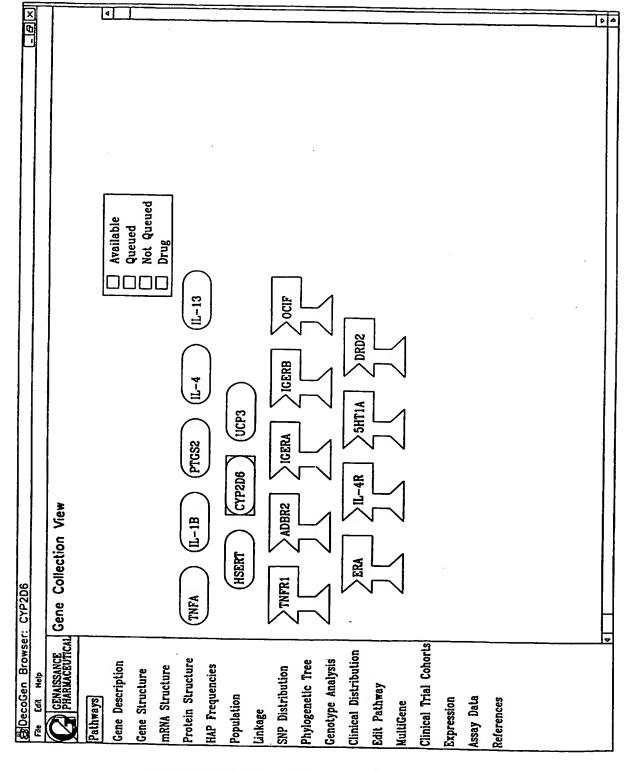


FIG. IA



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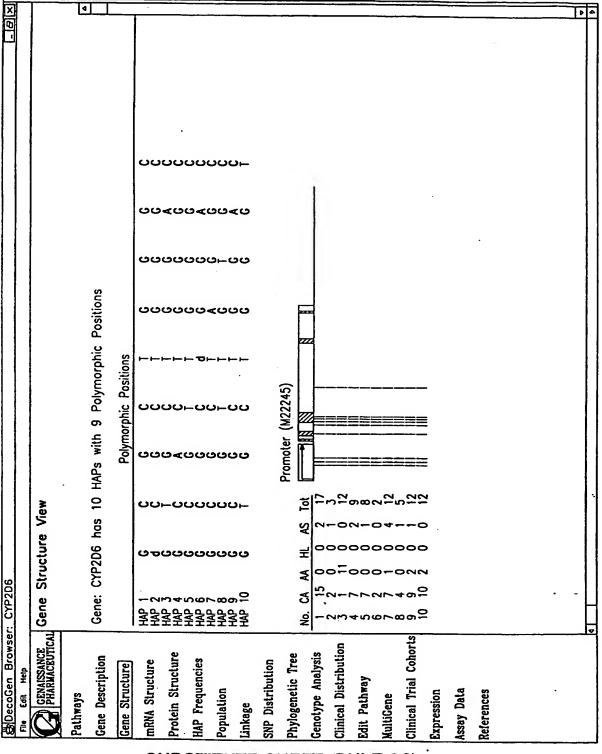
3/62 **N**



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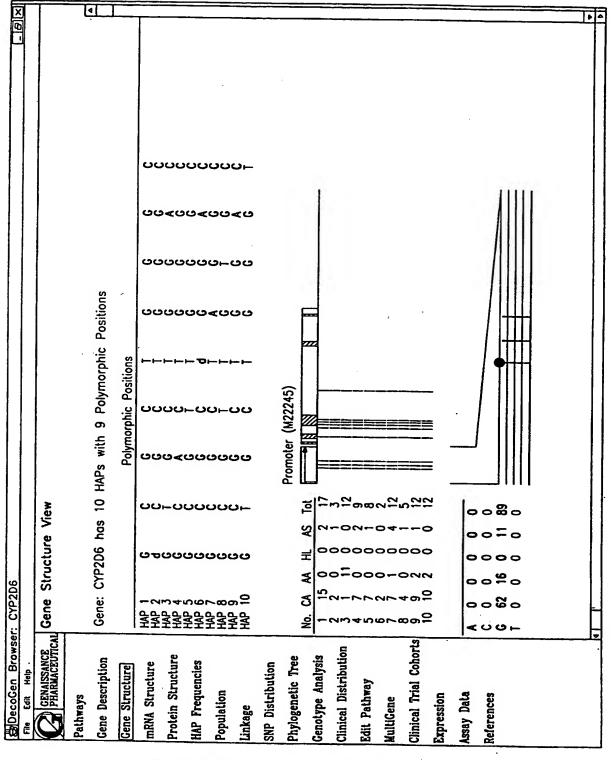
Salbecogen Browser: CYP206	CYP2D6		
File Edit Help			202
NCE	Gene Description View		
Pathways			
Cana Description	Name	CYP2D6	١٩١
Cene Structure	Definition	Human cytochrome P450 IID6 (CYP2D6) gene	<u>i</u> .
mena Structure	Function	Metabolic enzyme	
Profein Structure	Organism	Homo Sapiens	
HAP Frequencies	Length	9432	
Population	No Features	13	
linkage	Population Size	46	
SNP Distribution	No. Hoplotypes	10	
Phylogenetic Tree	Nucleotide Polymorphism (theta)	5.6E-4 +/- 3.1E-4	
Genotype Analysis	Nucleotide Diversity (pi)	2.85-4 +/- 1.85-4	
Clinical Distribution			
Edit Pathway			
MultiGene			
Clinical Trial Cohorts			
Expression	-		
Assay Data			
References			
·			
-			

FIG. 4₀ 5×5



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FIG. 4b 89/9



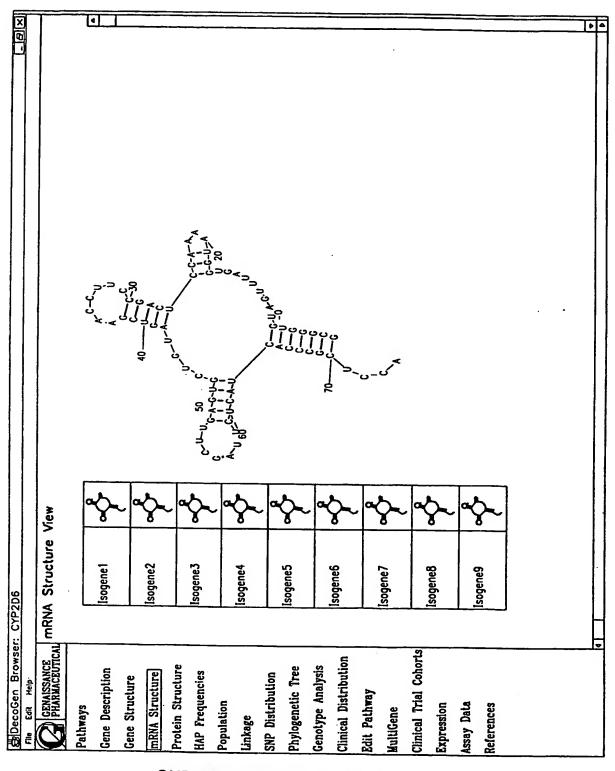
SUBSTITUTE SHEET (RULE 26)

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		520 530 540 550 560 500 500 600 600 600 600 600 60	Redrow
		580 tttctoatcog tttctoatcog tttctoatcog tttctoatcog tttctoatcog tttctoatcog tttctoatcog tttctoatcog	
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		560 steedageget steedageget steedageget steedageget steedageget steedageget steedageget steedageget steedageget	
	,	550 ccaaggatc ccaaggatc ccaaggatc ccaaggatc ccaaggatc ccaaggatc ccaaggatc ccaaggatc	
1388)		540 satatectgaa satatectgaa satatectgaa satatectgaa satatectgaa satatectgaa satatectgaa	
Gene (M33	4	530 atacogcaca atacogcaca atacogcaca otacogcac atacogcac atacogcac atacogcac	
<u>සු Cene Feature Sequence Alignment: Gene (M33388)</u>	olour Calculate Help	520 300000000000000000000000000000000000	
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ene	E	- 25450-80	g)
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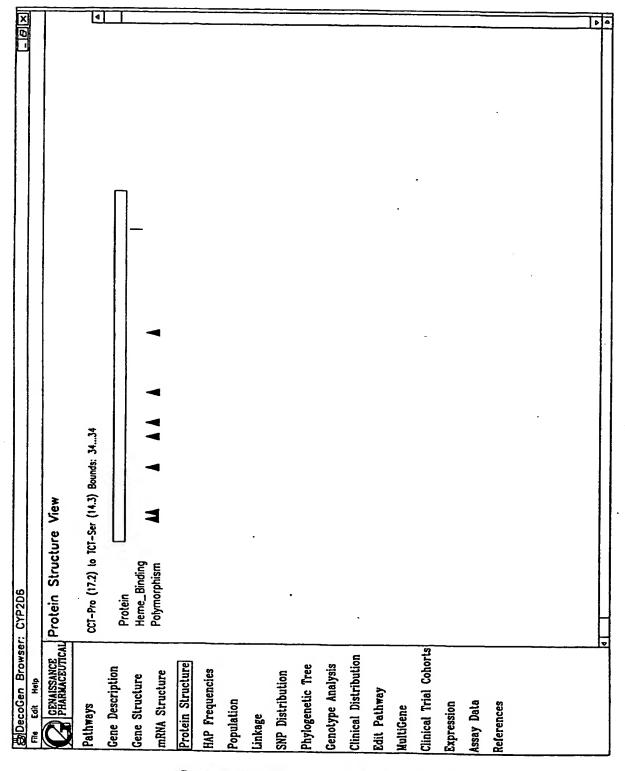
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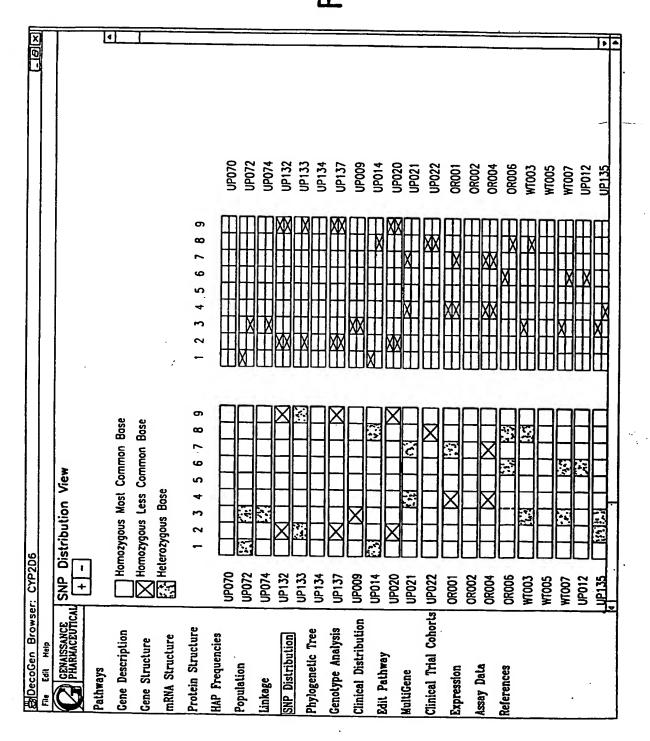
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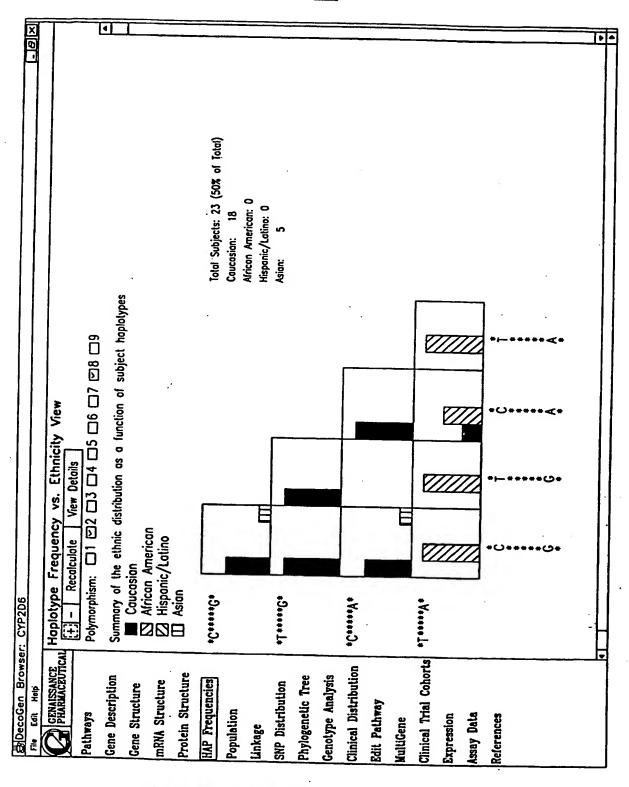
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思DecoGen Browser: CYP.	CYP206							XIE -
ARISSANCE ARMACEUTICAL	Population View	2						
Pathways	PID	Ethnicity	Age	Gender	HAP 1	HAP 2	Test	4
Gene Description	UP070	క	66	ᄕ	GCGCTGGGC	GCGCTGGGC	0.1	
Gene Structure	UP072	క	66	L.	decerecee	GCACTGGGC	0.2	
mRNA Structure	UP074	S	66	<u>u</u>	СССТСССС	GCACTGGGC	0.2	
Protein Structure	UP132	8	66	M	GTGCTGGGT	GTGCTGGGT	0.3	
HAP Frequencies	UP133	ర	66	М	GCGCTGGGC	GTGCTGGGT	0.2	
Population	UP134	S.	66	Ŀ .	GCCTGGGC	ссестеесс	0.1	
Linkage	UP137	ర	66	_≆	crecrecer	GTGCTGGGT	0.1	
SNP Distribution	UP009	క	66	<u>ı. </u>	GCACTGGGC	GCACTGGGC	0.1	
Phylogenetic Tree	UP014	ర	66	LL.	deecteece	GCGCTGGAC	0.3	
Genotype Analysis	UP020	ర	66	L.	стестесет	GTGCTGGGT	0.2	
Clinical Distribution	UP021	క	66	- ₹	сспстс	GCGCTGGGC	0.4	
Edit Pathway	UP022	క	66	3	GCCTGGAC	GCGCTGGAC	0.3	
MultiGene	08001	AS	88	∡	dccctccc	ссеттетес	0.2	
Clinical Trial Cohorts	OR002	ĄŞ	66	×	cccrccc	СССТСССС	0.3	
Expression	0R004	AS	66	u	CCACTGGGC	GCACTGGGC	0.2	
Assay Data	08006	AS	66	Ŀ	ссетсесс	GCGCTGGAC	0.1	
References	WT003	ర	66	LL.	сстссс	ссеттетес	0.2	
	WT005	క	66	×	ССТСССС	СССТСССС	0.2	
	WT007	క	66	2	сстстс	ссепстс	0.4	
	UP012	ర	66	u.	CCCTAGC	GCCTGCAC	0.1	
	UP135	క	66	2	GCACTGGGC	GCGCTGGAC	0.2	•
	-							1

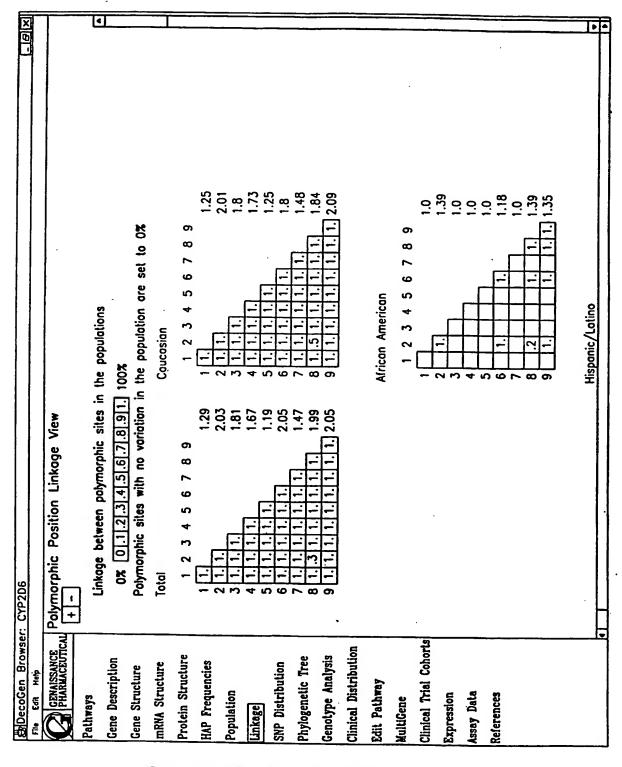


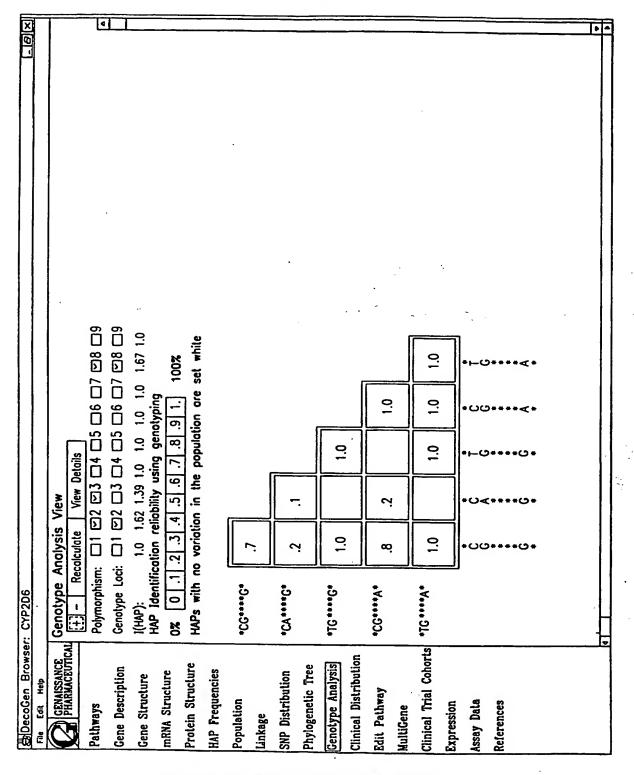
12 / 62 **O 9**



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BDecogen Browser:	: CYP206							9]-]	×Θ
File Edit Help					\ \				
GENAISSANCE PHARMACEUTICAL Pathways	Haplotype Frequency [+ - Recolculote Polymorphism: □1 □2	rency vs. Ethnicity View te [Vew Summary] l ⊡2 □3 □4 □5 □6 □7 ⊡8 □9	View □6 □7	□ 8 9	6		·		٠
Gene Description	Details of the ethnic	of the ethnic distribution as a function of subject haplotypes	tion of sut	bject hop	olotypes				П
Gene Structure mRNA Structure	3 Columns and Total numb	Columns are given for each Ethnogeographic group: Total number sampled with HAP poir	geographic air	group:					
Protein Structure	Fraction of Fraction ex	Fraction of the ethnogeographic group with that HAP pair Fraction expected under Hordy—Weinberg equilibrium for that HAP pair	roup with tinberg equi	thot HAP	poir or that HAP pair				
HAP Frequencies	HAP 1	HAP 2	z	XPop.	Caucasion	African American	Hispanic/Latino	ino Asi	
Population	*9*****0*	*9******	23	20%	18 56.3% 37.9%	29.0 20.0 0	0 0.02 0.02		_
Linkage	**********	*O****O*	7	4%	6.3%	0 0.0% 2.4%	0 0.0% 0.0%	00	
CND Diet ribution	* * * * * * * * * * * * * * * * * * * *	*******	+ ~	10%	4 12 52 25 22	% 0.0 0.0	% C		==
Sir Martinghom	*C********	*V************************************	ט רי	229	9.4%	0.0%	200		
Phylogenetic Tree	* V***** L*	*9******		2%	0.0%	12.5%	0.0%		_
Genotype Analysis	* V * * * * L *	*O*****L*	77	% 5	0 0.0% 0.8%	25.0%	0 0.0% 0.0%		
Clinical Distribution	*V*****L*	*V****L*	ח ר	5 %	0 0.0% 0.1%		0.0%		
Edit Pathway									==
MultiGene									
Clinical Trial Cohorts									==
Expression									_
Assay Data									
References									==
_12									0 -
									1





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BDecoGen Browser: (: CYP206					É
File Edit Hetp					713)	
GENAISSANCE PHARMACEUTICAL	Genotype Analysis View	llysis View				1
Pathways	Polymorphism:			6 		•
Gene Description	Genotype Loci:	04 05		6 □ 8 □ 9		•
Gene Structure	I(HAP):	1.0 1.56 1.0 1.0 1.0 1.0	1.0 1.6	1.0		
mRNA Structure	HAP 1	HAP 2	2	TD00		
Protein Structure	*S*********	*9************	23	50%	100%	T
HAP Frequencies	*O***** L*	**************************************	7 4	24 % 2%	100%	
Population	*C*****	********	. ი	10%	2001	_
Linkage	*C****************	* V * * *	m -	24	100%	
ribintion	* V * * * * L *	*9**** L*	- 6	47	1003	
	*V***** L*	*C*****	ı ••>	29	100%	
Phylogenetic Tree	* V***** L*	* V**** L*	٣	29	100%	
Genotype Analysis						
Clinical Distribution						
Edit Pathway						
MultiGene						
Clinical Trial Cohorts						
Expression						
Assay Data						
References						
				•		
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17 / 62 <u>9</u> <u>9</u>

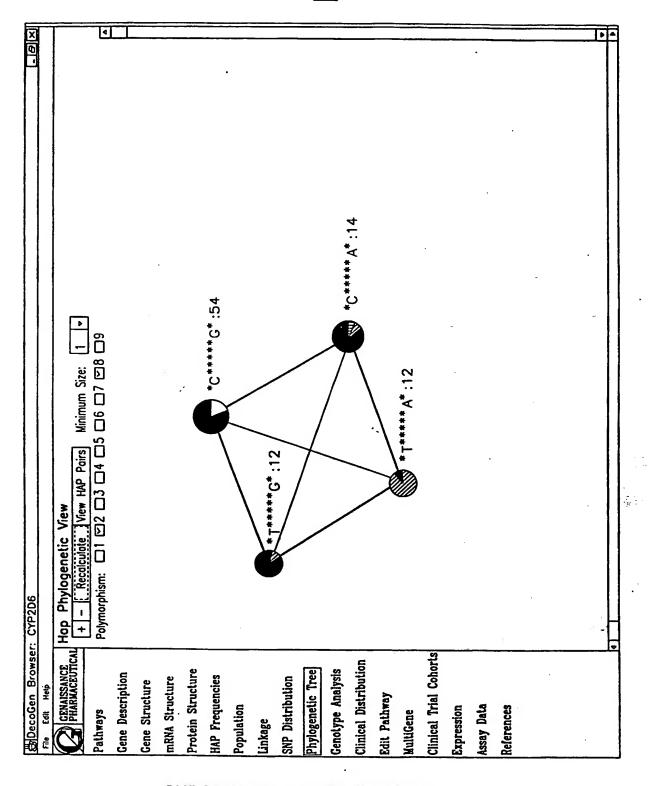
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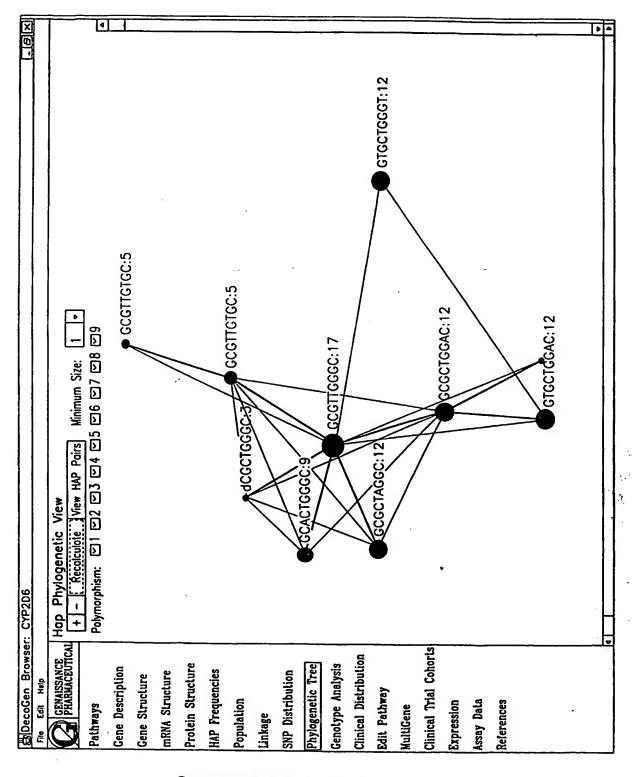
 Polymorphism: □1 □2 □3 □4 □5 □6 □7 □8 □9

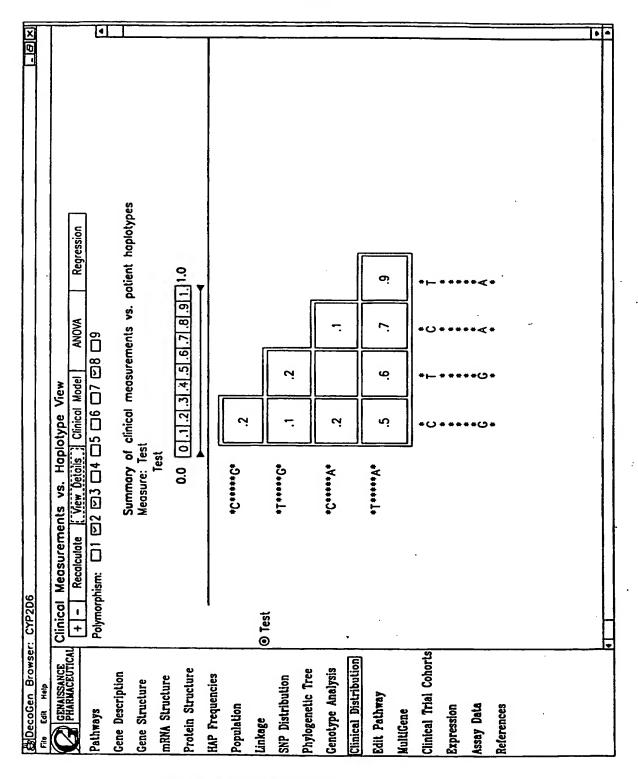
 Pasitive 1.0 1.56 1.0 1.0 1.0 1.0 1.0 1.6 100% 100% 100% 100% 100% 100% ******** *C***** * V * * * * L * Genotype Analysis View HAP 1 *C*****G* *D***** L* *C***** *9***** L* *C***** * Y***** L* * Y * * * * L * 본)DecoGen Browser: CYP2D6 I(HAP): GENAISSANCE PHARMACEUTICAL Clinical Trial Cohorts Clinical Distribution Protein Structure Genotype Analysis Phylogenetic Tree Gene Description HAP Frequencies mRNA Structure SNP Distribution Gene Structure Edit Help Edit Pathway Population Pathways Assay Data MultiGene Expression References Linkage

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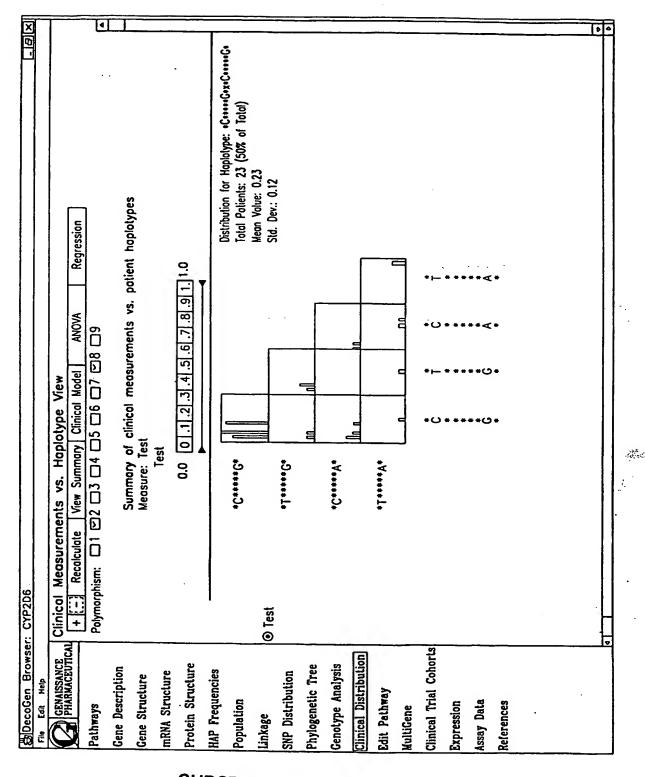
19 / 62 **19** .





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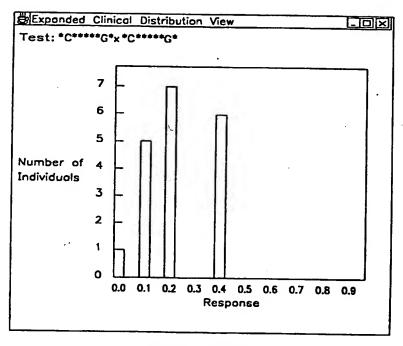


FIG. 20

Site	Slope	Intercept	Variance	T(slope)	Significance Level	
ı	-0.083	0.316	0.05	-0.59	0.7223	
2	0.154	0.231	0.04	4.22	0.9999	
5	-0.08	0.326	0.05	-1.16	0.8735	
;	-0.0080	0.313	0.06	-0.14	0.5572	
i	0.145	0.305	0.05	0.86	0.804	
i	-0.08	0.332	0.05	-1.24	0.890 <u>2</u> *	
,	0.0070	0.31	0.06	0.08	0.5303	
3	0.158	0.222	0.04	4.34	1.0	
}	-0.043	0.322	0.05	-0.76	0.7752	

FIG. 21

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Bocogen Browser: CYP	r: CYP2D6								XIØI-I
File Edil Help									
GENAISSANCE PHARMACEUTICAL	_	Measurements vs. Haplotype View Recalculate (View Distribution) Clinical Model	Haplotype View		Regression	! !			
Pathways	Polymorph	Polymorphism: □1 ⊡2 □3 □4 □5 □6 □7 ⊡8 □9	5 □ 6 □ 7 ⊡ 8 □ 9						•
Gene Description		Summary of	Summary of clinical measurements vs. patient haplotypes	s. patient	haplotype	s,			
Gene Structure		Meosure: Test	**	-					
mRNA Structure		lest							
Protein Structure		0.0	0 . 1 . 2 . 3 . 4 . 5 . 6 . 7 . 8	0.1_10					· · ·
HAP Frequencies	ļ			,					
	O Test	HAP 1	Hop 2	Z	%Pop.	Mean	Stddev)	X2	0(x • 2 K-3)
Linkage		*9******	********	23	20%	0.24		9.17	0.0 (1)
SNP Distribution			*O*****O*	7	4 6 % 8	0.15		0.0	_
Phylogenetic Tree		*V*********	*5*************************************	Գ ռ	2% 10%	0.2	0.08	2 K	0. C
2011		*C*****A*	*C*****	· 17	289	0.13		0.0	_
Genotype Analysis		*V*****L*	*9******	-	2%	0.5		0.0	_
Clinical Distribution		*V****L*	*9****L*	7	4%	0.55	_	0.0	_
Edit Pathway		• V • • • · · · · · ·	*C*****A*	נא נא	2 2 2 2	.6 0.93	0.1	0 0	1.0 (5-) (5-)
MultiGene				•				}	_
Clinical Trial Cohorts									-
Expression									
Assay Data	⊙ Test								
References									
									Þ

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	osur ments				
olymorphism	: 🗆1 🖾2 🗀	3 🗀 4 E	⊃5 □ 6 □	コ7 図8 🗀 9	
Source of Va	riation DF	Mean Squar	res F-ratio		1
Between Grou	ps 7	0.26	19.65		
Within Groups	37	0.01	13.05		
Critical F-Dis	tribution Value 90	Z- 1 88			-
	tribution Value 955				
	tribution Value 99				
	tween-group varia				
Significant be	tween-group varia	tion at the	95% confide	nce level	
Significant be		tion at the	95% confide	nce level	
Significant be Significant be	tween-group varia tween-group varia	tion at the tion at the	95% confide 99% confide	nce level nce level	
Significant be Significant be	tween-group varia tween-group varia HAP 2	tion at the tion at the N	95% confide 99% confide Average	nce level nce level Std. Dev.	_ 1
Significant be Significant be HAP 1 *C*****G*	tween-group varia HAP 2 *C*****G*	tion at the tion at the N 23	95% confide 99% confide Average 0.23	nce level nce level Std. Dev. 0.12	_
Significant be Significant be HAP 1 *C*****G*	tween-group varia HAP 2 *C*****G* *T*****G*	tion at the tion at the N 23 2	95% confide 99% confide Average 0.23 0.15	Std. Dev. 0.12 0.07	_
Significant be Significant be HAP 1 • C*****C* • C*****C*	tween-group varia HAP 2 *C*****G* *C*****A*	tion at the tion at the N 23 2 5	95% confide 99% confide Average 0.23	nce level nce level Std. Dev. 0.12	- 1
Significant be Significant be HAP 1 •C*****G* •C*****G* •C*****G*	tween-group varia HAP 2 *C*****G* *C*****A* *T*****G*	tion at the tion at the N 23 2	95% confide 99% confide Average 0.23 0.15	Std. Dev. 0.12 0.07	-
Significant be Significant be HAP 1 • C******G* • C*****G* • C*****G* • T*****G* • T*****G*	tween-group varia HAP 2 *C*****G* *C*****A*	tion at the tion at the N 23 2 5	95% confide 99% confide Average 0.23 0.15 0.22	Std. Dev. 0.12 0.07 0.13	-
Significant be Significant be HAP 1 •C*****G* •C*****G* •C*****G*	tween-group varia HAP 2 *C*****G* *C*****A* *T*****G*	tion at the tion at the N 23 2 5 4	95% confide 99% confide Average 0.23 0.15 0.22 0.2	Std. Dev. 0.12 0.07 0.13 0.08	-
Significant be Significant be HAP 1 • C******G* • C*****G* • C*****G* • T*****G* • T*****G*	tween-group varia HAP 2 *C*****G* *C*****G* *C*********** *T**********	tion at the tion at the N 23 2 5 4 2	95% confide 99% confide Average 0.23 0.15 0.22 0.2	Std. Dev. 0.12 0.07 0.13 0.08 0.07	
Significant be Significant be HAP 1 • C******G* • C******G* • T*****G* • T*****G* • C******G* • C******A*	tween-group varia HAP 2 *C*****G* *T*****G* *T*****G* *T*****A*	tion at the tion at the N 23 2 5 4 2 3 3	95% confide 99% confide Average 0.23 0.15 0.22 0.2 0.55 0.13	Std. Dev. 0.12 0.07 0.13 0.08 0.07 0.15	

FIG. 23

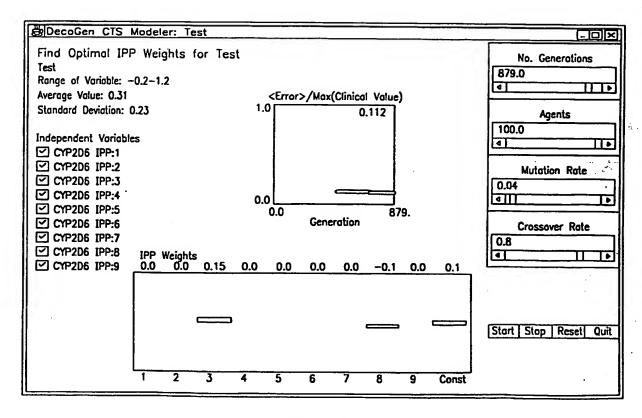
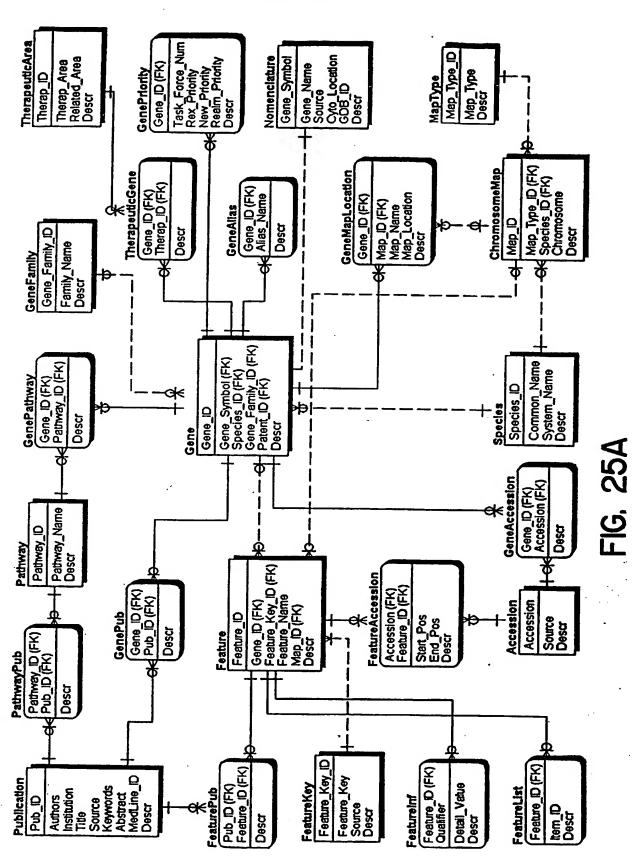
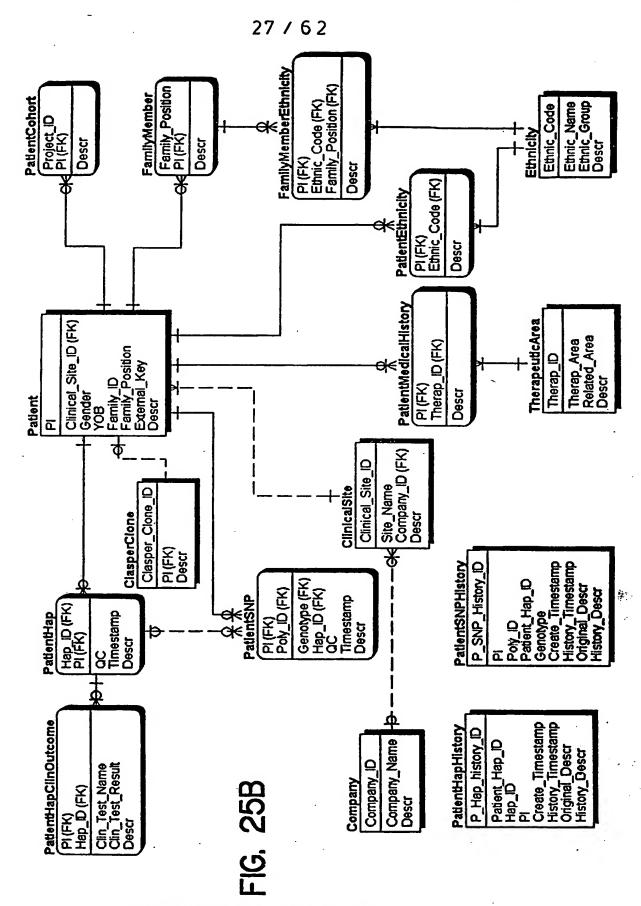


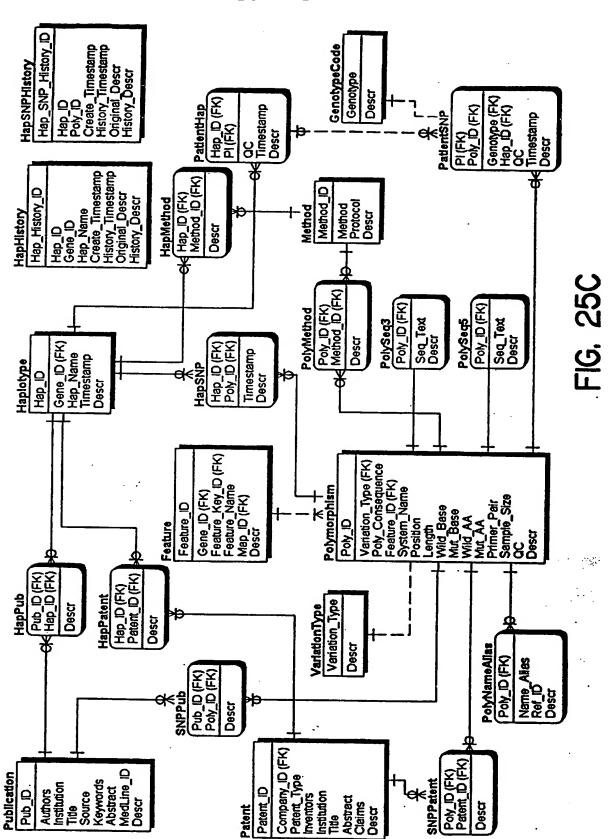
FIG. 24
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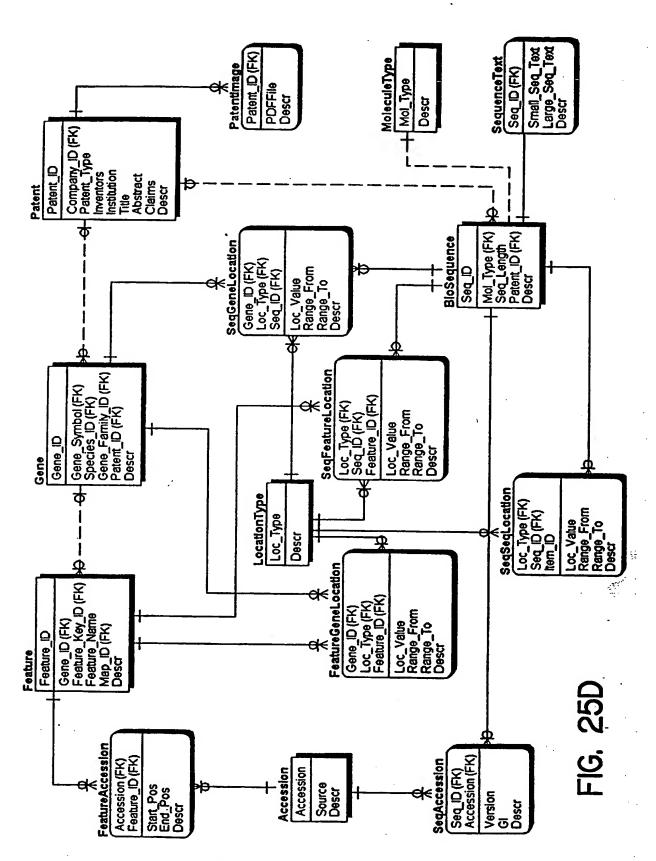
SUBSTITUTE SHEET (RULE 26)



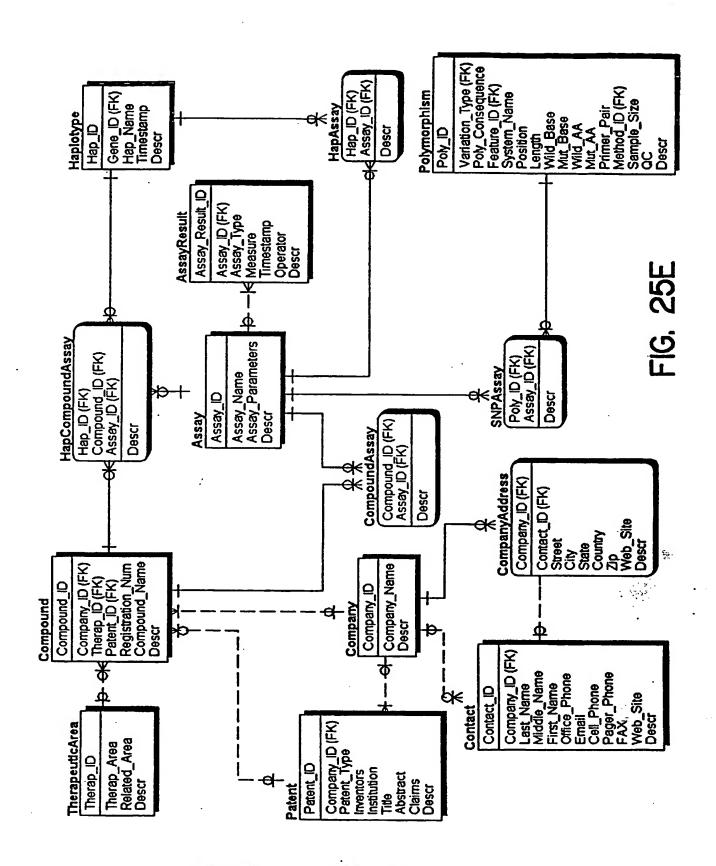
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Legend of Figures:



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Rectangle Boxes: Tables in the database.



Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

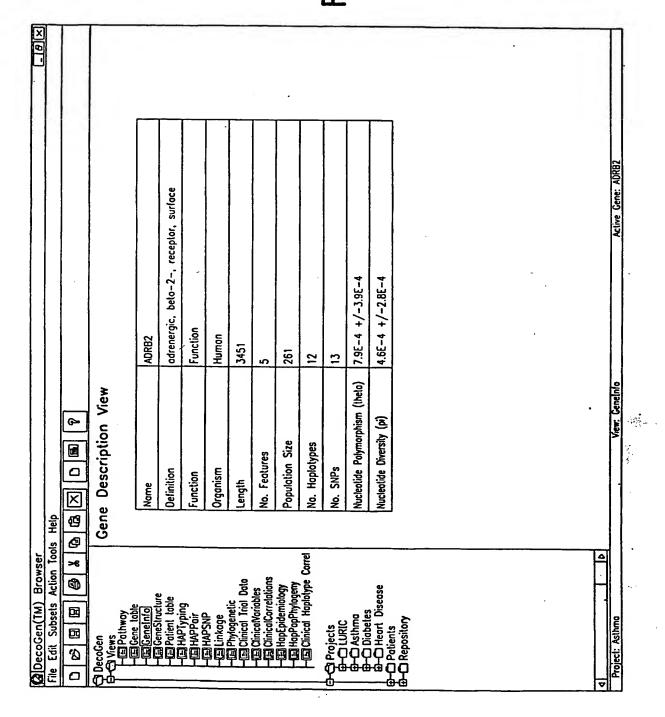
- 2: Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 10: |------ Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 12: --- Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-exact-1 relationship.
- 14: $+--\Leftrightarrow$ Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.

FIG. 25F

-1G. **2**%

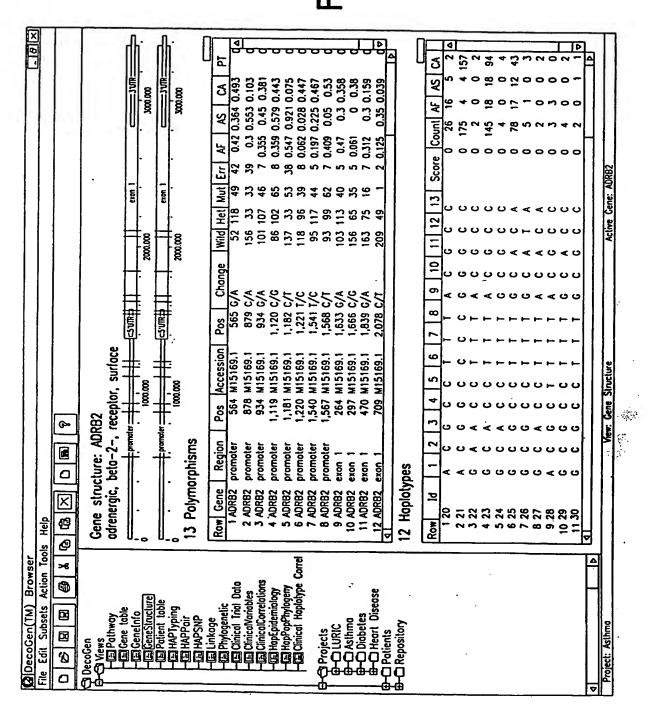
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	& © O	Asthma Extracellular OADBR2	Introcellular	OPDEGB	OCALM1	
ObecoGen(TM) Browser File Edit Subsets Action Tools Help		Concocen Concocen Concocen Concocente Concoc	La Unicorvandones La UnicorCorrelations La Happigemiology	Clinical Haplotype Carrel	P-10 LURIC P-Clasthmal	<u>A</u>

FIG. 27



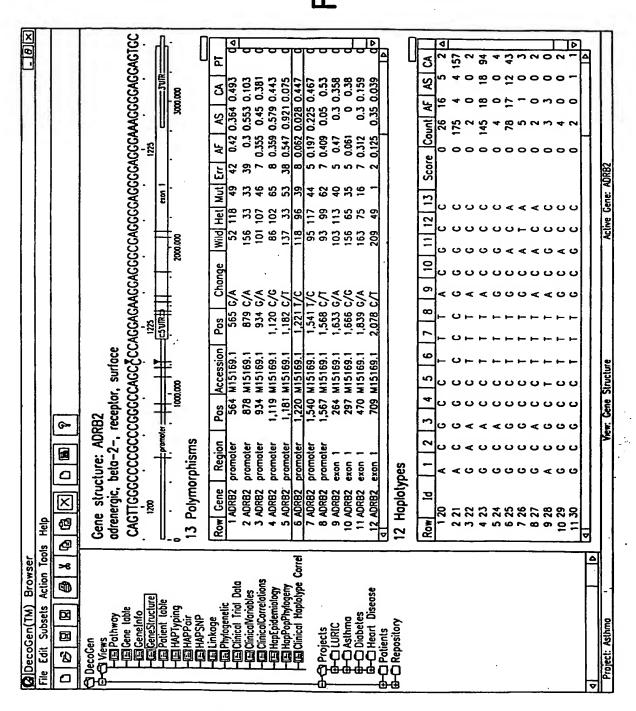
SUBSTITUTE SHEET (RULE 26)

FIG. 28A



SUBSTITUTE SHEET (RULE 26)

FIG. 28B



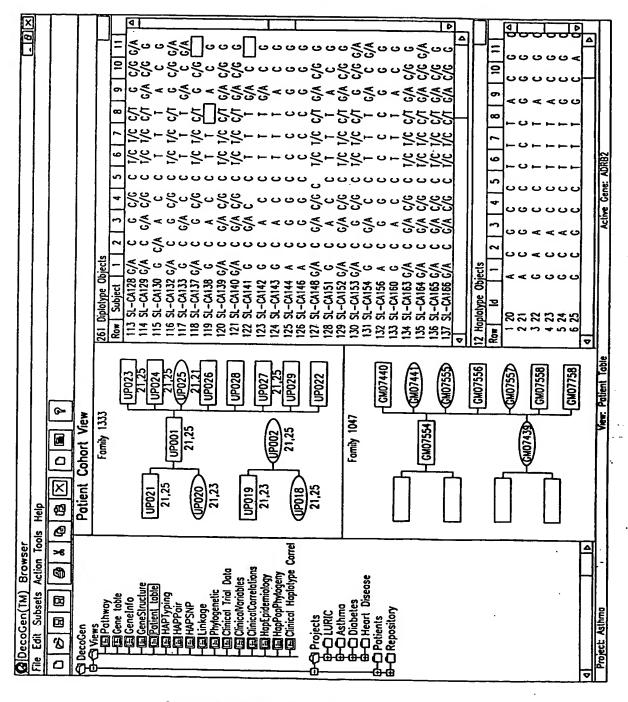
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IG. 29A

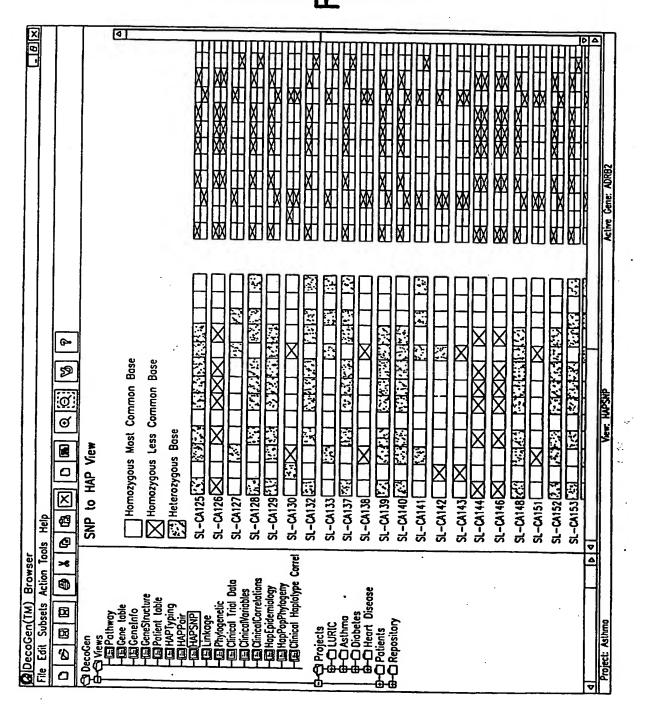


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(A) DecoGen(TM) Browser											N N
File Edit Subsets Action Tools	ıls Heip										
		6 →									
G DecoGen	Clinical Trial D	Data									
LE Pothers	182 PatientMeosurement Objects	nt Objects									L
	Row Potient	Severily	Severily Skin Tes FVC LP	FVC LP	IVC ZP	נגאור	FEV1 %	. FEV1/FV	FEF PRE	FEF %P	2
Genelufo	1 SL-AA131	2.0	1.0	1.88	58.0	1.28	52.0	68.0	0.8		1.8.4
—(★) GeneStructure	2 SL-AA134	2.0	1.0	2.01	54.0	96.0	34.0	48.0	0.45	Ì	2.2
Polient toble	3 SL-A4136	0.0	0.0	2.56	89.0	2.22	93.0	87.0	3.2	91.0	2.5
HE HAPTyping		2.0	1.0	1.4	50.0	9.6	27.0	43.0	0.22		1.5
Talka Par	5 SL-AA155	2.0	0.	1.77	40.0	0.98	27.0	55.0	0.61		2.2
TAPONE STORY	6 SL - AA159	2.0		2.89	0.99	1.71	51.0	59.0	6.0	20.0	4.4
TEST CHINGS	7 SL-AA195	0.		4.28	96.0	2.7	79.0	63.0	1.48	33.0	5.2
CE Charce Trial Data	8 SL-AA211	0.		3.44	91.0	1.97	0.99	57.0	1.39	32.0	5.5
The Civicol Cold	9 SL-AA227			1.93	54.0	96.0	37.0	49.0	0.35	0.11	2.5
(in Clinical Correlations)		0.	0:	3.0	96.0	2.01	70.0	57.0	0.99	25.0	3.8
Han Fordeminion	=			NP	dΝ	Νb	dN	θN	<u>N</u>	dN	<u>Q</u>
TE HooPooPhylogeny	12	<u>Q</u>		NP	dN	dN	NP	d N	d.	g.	9
TE Clinical Hoplotype Correl	13	1.0	1.0	2.17	85.0	1.92	64.0	71.0	1.33	38.0	3.2
	=	2.0	1.0	3.56	29.0	2.16	46.0	61.0	1.13	18.0	1.
(하스) Projects	15 SL-CA104		0.0		57.0	1.46	39.0	53.0	0.59	16.0	3.4
e-O LURIC					62.0	1.11	46.0	57.0	0.55	24.0	2.3
E-C) Asthmo	17 SL-CA106	0.0		3.46	82.0	5.69	83.0	57.0	2.28	51.0	4.
Diobetes	18 SL-CA107			3.82	113.0	2.59	83.0	78.0	1.7	46.0	3.9
	19 St -CA108				₽	ջ	Q.	٩	NP	NP	NP
Potients	20 StCA109	0.1		Ī	93.0	1.7	7.0	64.5	0.89	25.0	2.8
ET Kepository	21SL-CA110	8			114.0	3.18	101.0	70.0	2.24	51.0	4.5
	22 SL-CA111			3.08	69.0	2.01	58.0	65.0	1.12	32.0	3.3
	23 SL-CA114				84.0	2.18	77.0	77.0	1.77	43.0	3.0
	24 SL-CA116				83.0	1.91	79.0	78.0	1.8	49.0	2.4
	25 SL-CA117	<u>e:</u>			90.0	2.25	67.0	59.0		22.0	<u>-</u>
	26 SL-CA118			1.53	76.0	1.27	71.0	83.0	1.27	49.0	9.
,	27 St-CA119				dN	dN	dΝ	dΝ	dN	dΝ	9
	28 St - CA120	7			106.0	17.7	83.0	64.0	191	33.0	4.4
	29 SL-CA121				88.0	1.9	70.0	62.0			3.6
	30 SL-CA122				105.0	4.35	103.0	75.5	3.52	62.0	0.0
	31 SL-CA123				0.99	0.92	40.0	50.0		Γ	2.5
	32 SL-CA124			2.45	29.0	1.3	43.0	53.0	0.41	0.11	2.5
	33SL-CA125				42.0	0.81	37.0		0.47	22.0	<u></u>
	34 St - CA126		1		64.0	1.17	52.0				8.
	4 SISI - CA127	9	9	197	68.7	163	1330	1830		9 99	26.9
Project: Aethmo		1 1 1 N	Van: Change Land Bate				,	4000			3
Common and the common		VIEW. CHI		2			Active Gene: AUKB2	AUKBZ			٦
	•									•	

FIG. 30



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FIG. 3

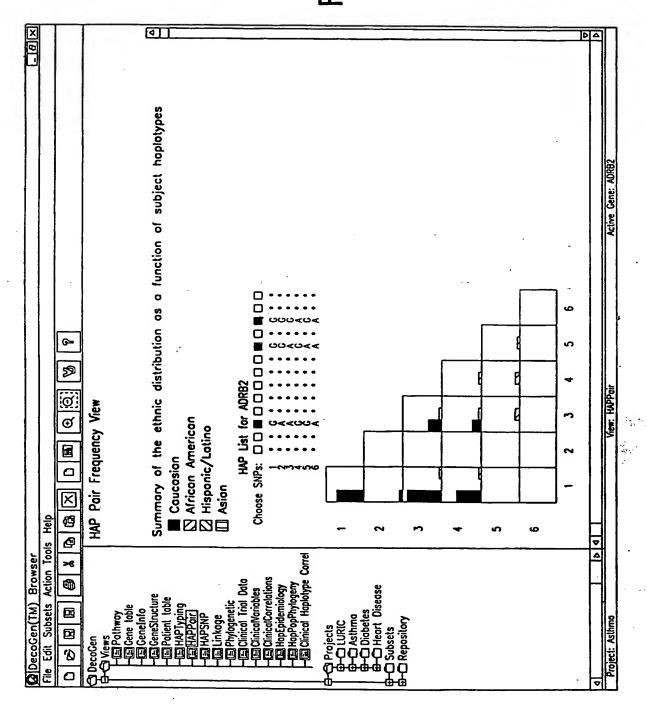


FIG. 32

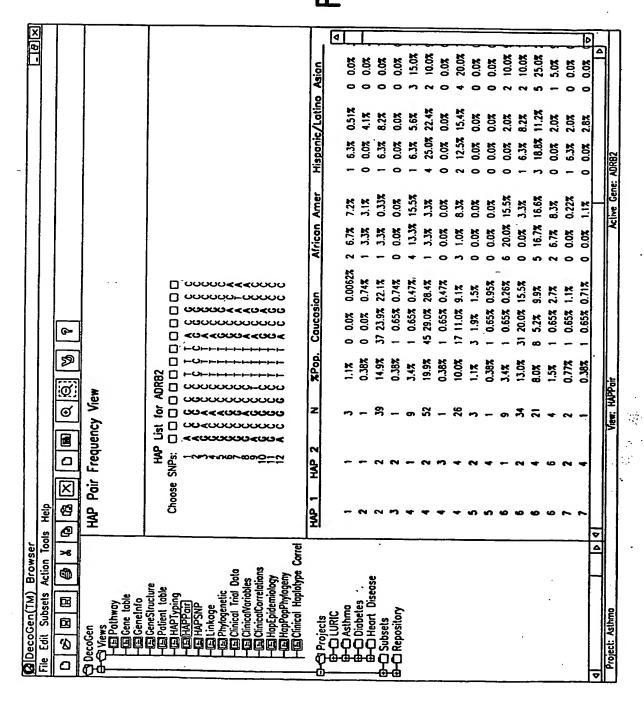
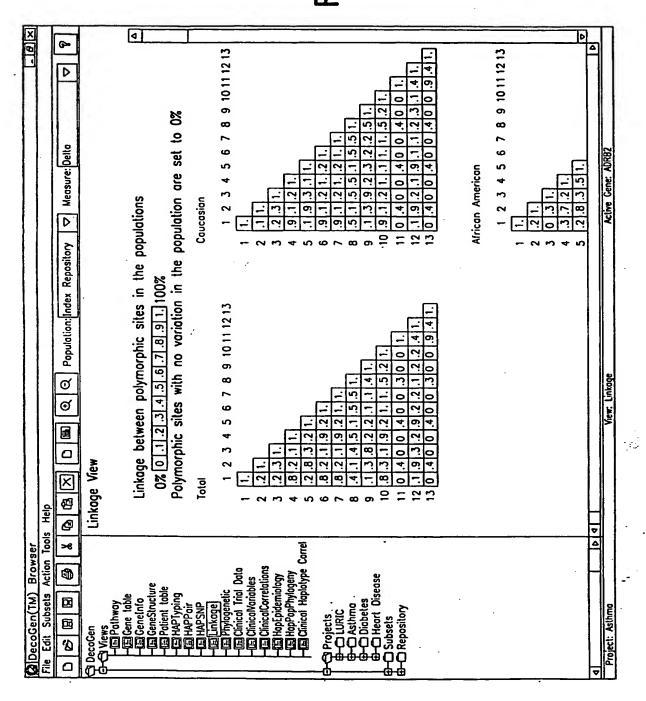
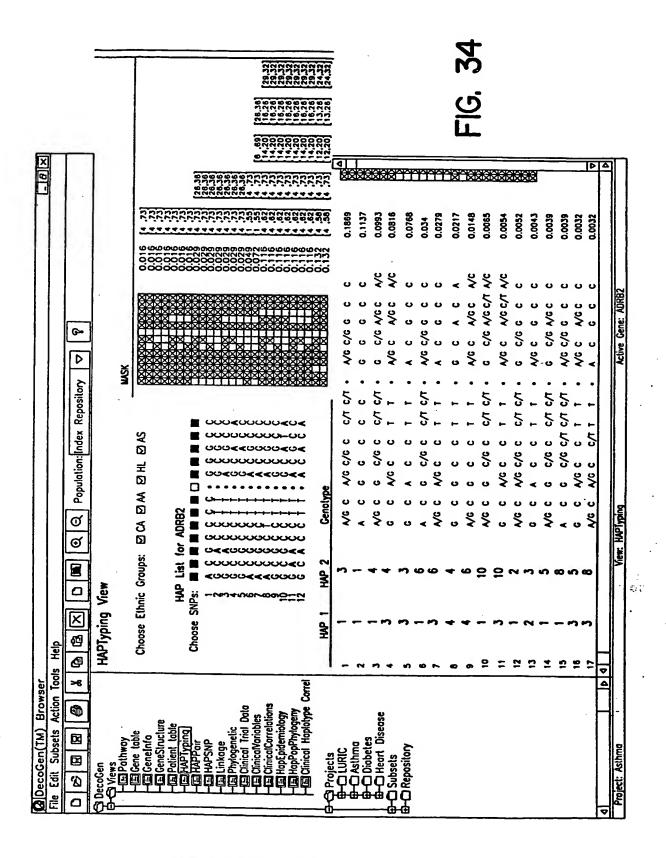


FIG. 3

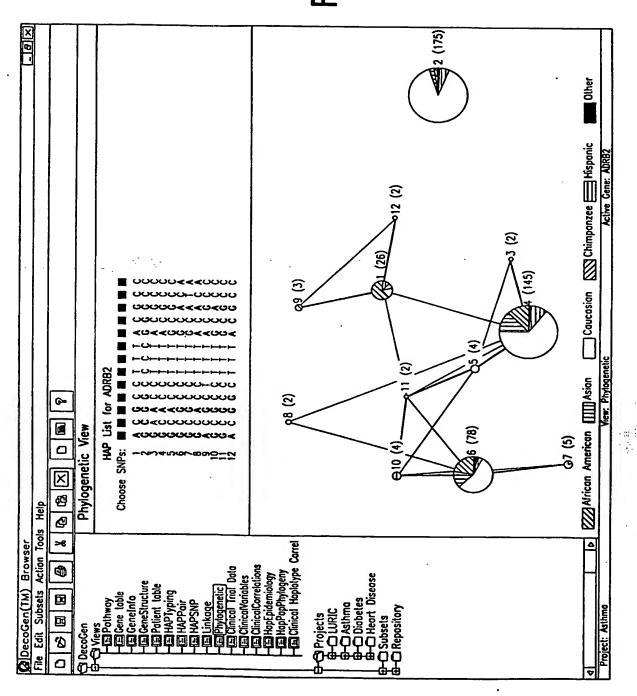


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SUBSTITUTE SHEET (RULE 26)

FIG. 35



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44/62

FIG. 36

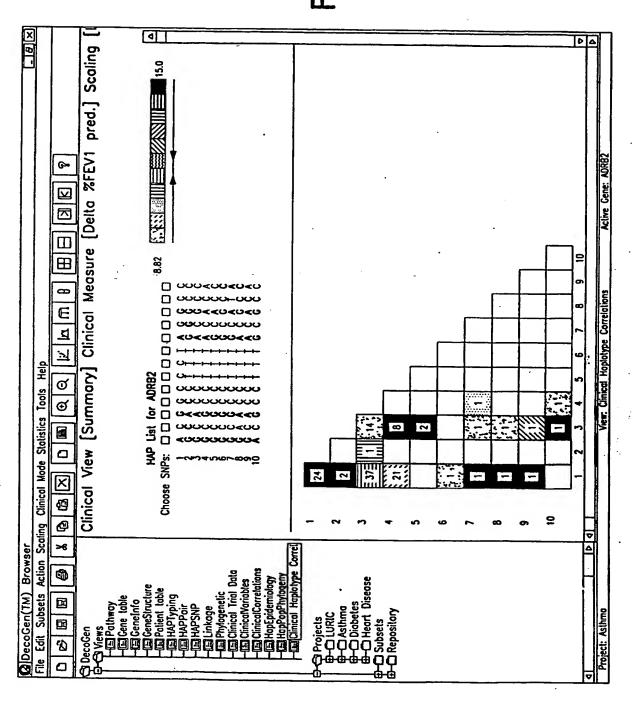
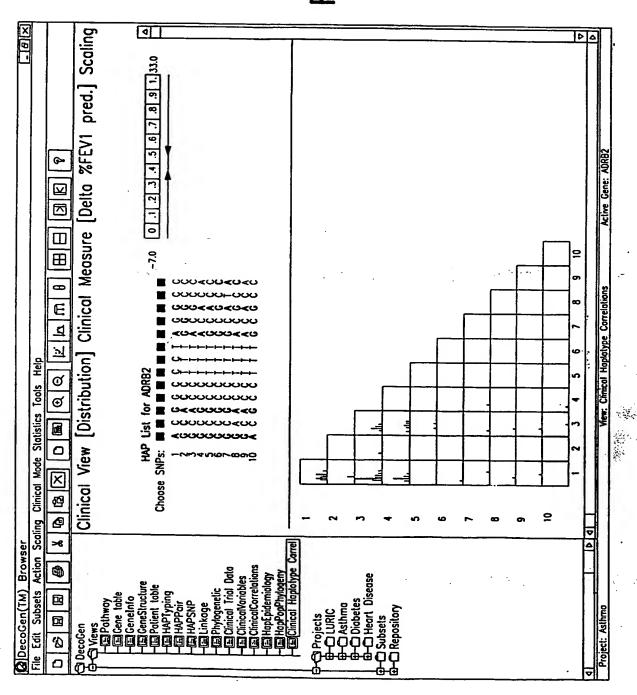


FIG. 37



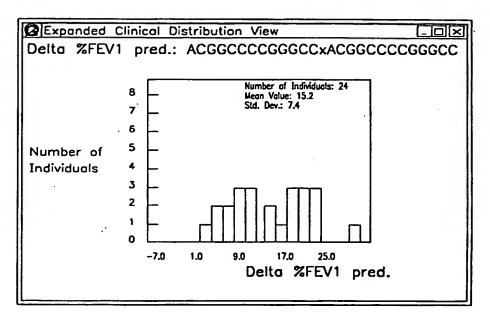


FIG. 38

DecoGen Single Ge	ne Statistics	Calculato	r				-	
File								
Show/Hide	CC Line	<u> </u>						
Gene: adrenergic,	beta-2-, 6	eceptor.	surface	Clinic	al Meas	ure: Delta %	FEV1 pro	ed.
			Confidence:	0.05 0.1	Fixed Si	ite: -4		
Regression Res	ults							<u> </u>
Marker	Intercept	Slope	Stope Ran	ige	R** 2	Corr. Coef (R)	P-value	
*G******	10.501	1.99	-0.08	4.06	0.0301	0.1734	0.0297	
	10.526	1.956	-0.11	4.02	0.0293	0.1711	0.0314	
□*******A*G**	14.583	-2.206	-4.28	-0.13	0.0365	-0.1911	0.0187	- 1.
□**A****A****	14.471 14.626	-2.048	-4.13 -4.32	0.032 -0.16	0.0315 0.0374	-0.1774	0.0268	
□**A*****G**	14.615	-2.241 -2.308	→.32 -4.4	-0.16 -0.21 ~	0.0374	-0.1934 -0.1977	0.0175 0.0156	
GCACCTTTACGCC	14.6	-2.343	-4.46	-0.22	0.0394	-0.1984	0.0153	
		4.5.15		V			0.0.00	
	·							
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Lancine -								.
4								

FIG. 39A

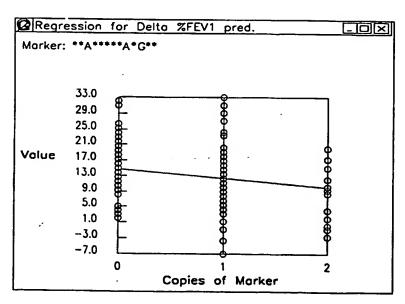
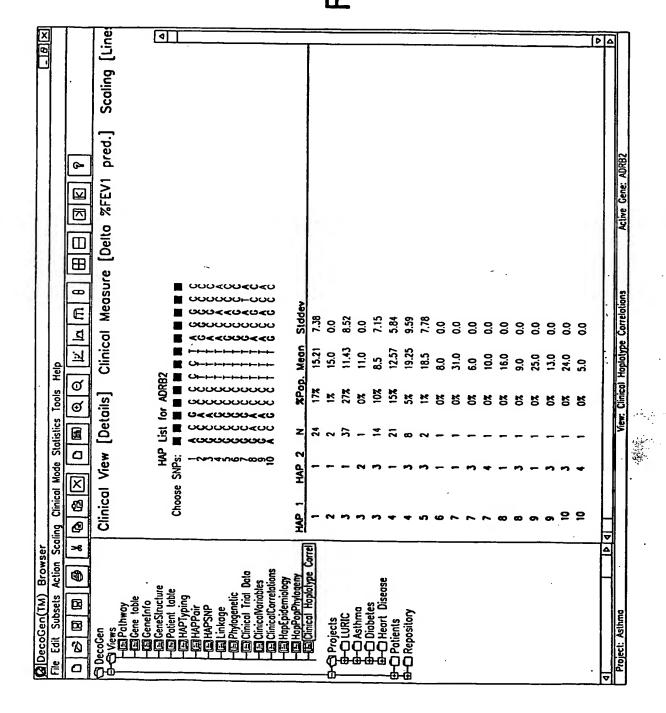


FIG. 39B

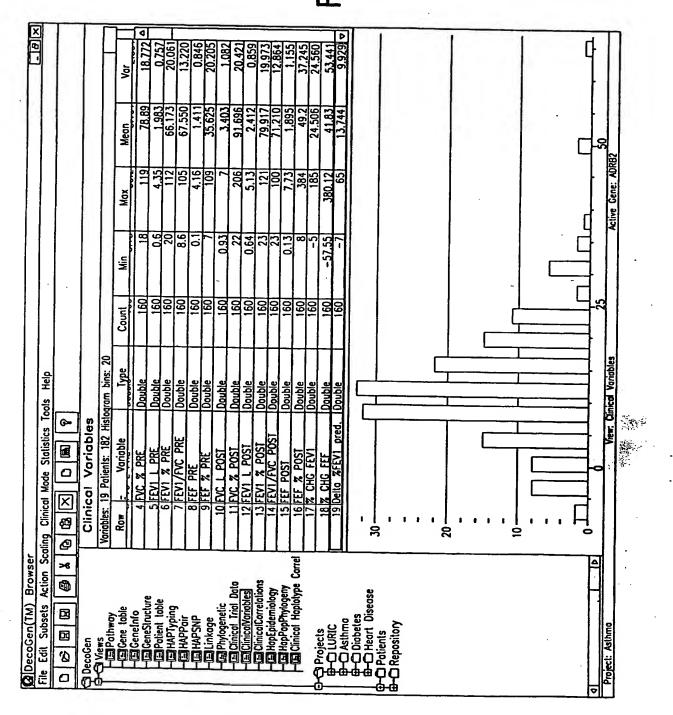
FIG. 40



DecoGen Single	Gene Stat	istics Calculate	or		-0
ile					
<u>a</u> Q Q					
linical Measure	ments A	NOVA Calcula	tion		
Source of Variation	OF	Mean Squares	F-ratio	_	
Between Groups	6	145.83	2.49		
Within Groups	101	58.59	2.49		
P-value for signific	once: 0.02	7		-	
	for ADRB2	2			
Choose SNPs:					
₹ Ĝ }	;	118888	ζ	•	
4 G	: ĉ	1 1 6 6 4 6	C <u>A</u>		
\$ \$ }	: & & & t	† † 6 × × × × × × × × × × × × × × × × ×	E		
**************************************		XXXXXX-CXX XXXXXXXXXXX XXXXXXXXXXXX XXXXXXXX	Ă Ĉ Ĉ		
	13333	3 3 3 3 4 F	É		
HAP 1 HAP	2	N	Average	Std. Dev.	
1 1		24	15.21	7.38	
1 2		2	15.0	0.0	
1 3		37	11.43	8.52	1
1 4		21	12.57	5.84	1
3 3		14	8.5	7.15	
3 4		8	19.25	9.59	
3 5		2	18.5	7.78	
			···		

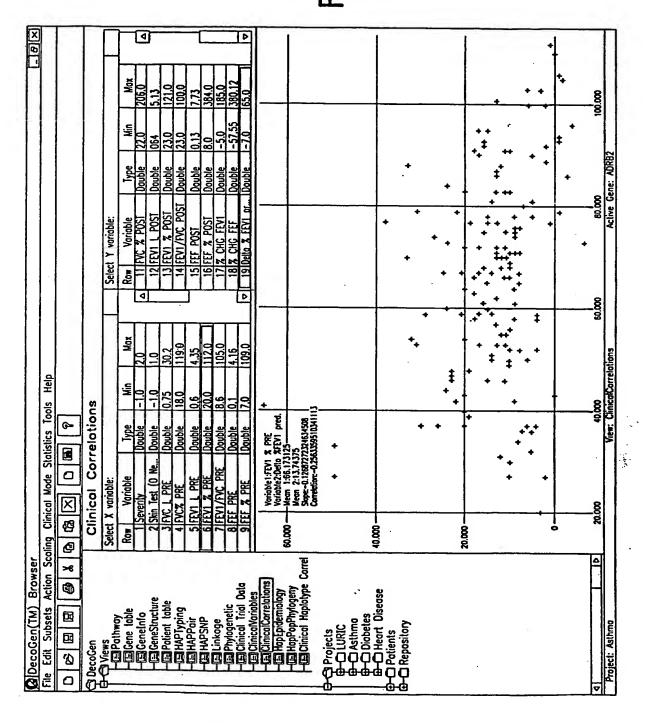
FIG. 41

FIG. 42

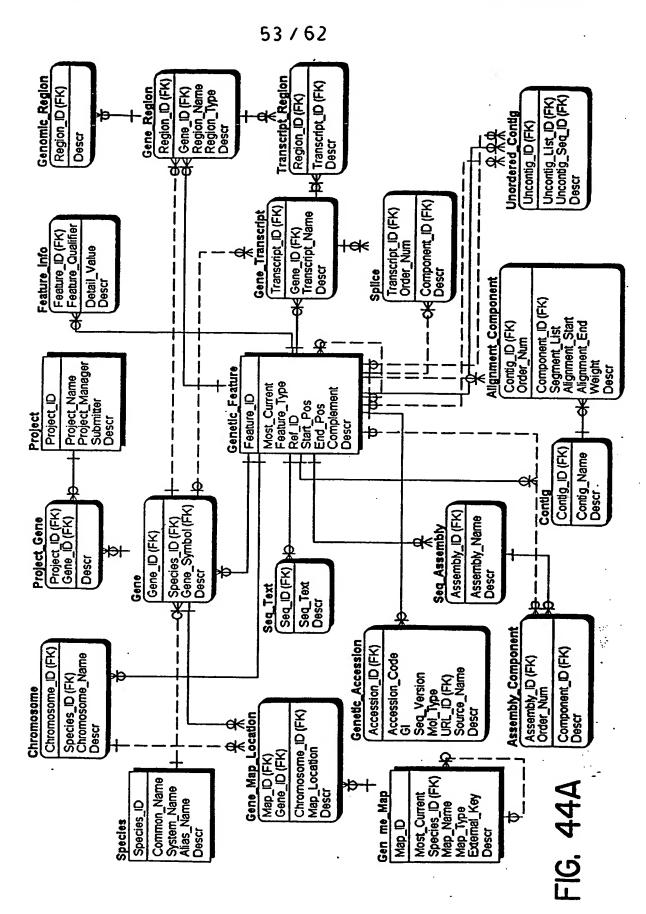


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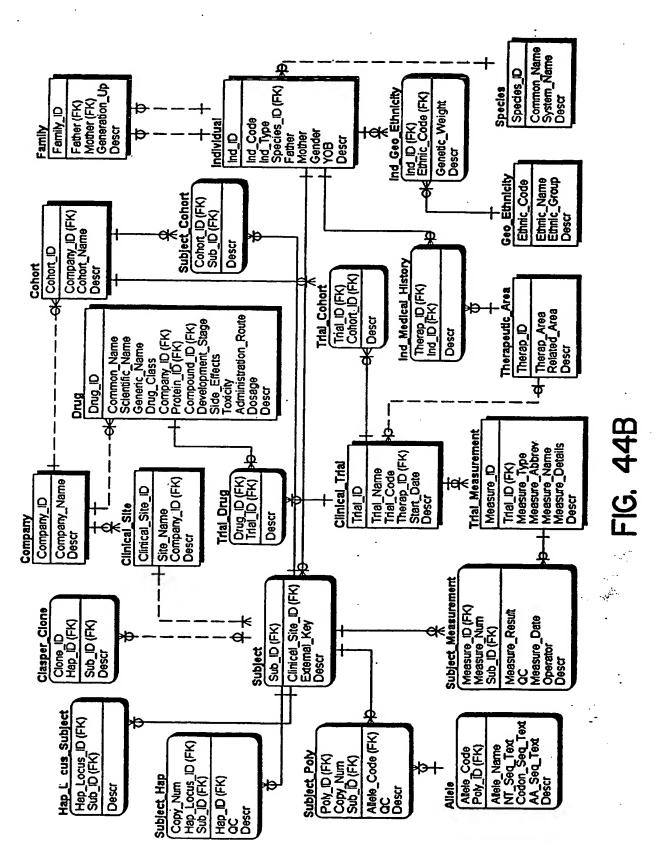
FIG. **4**:



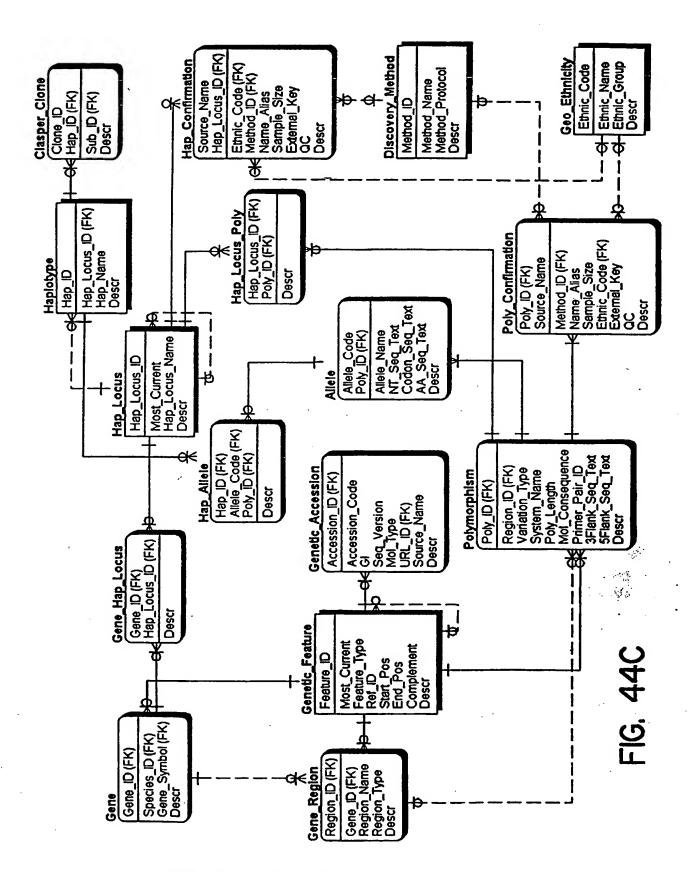
SUBSTITUTE SHEET (RULE 26)



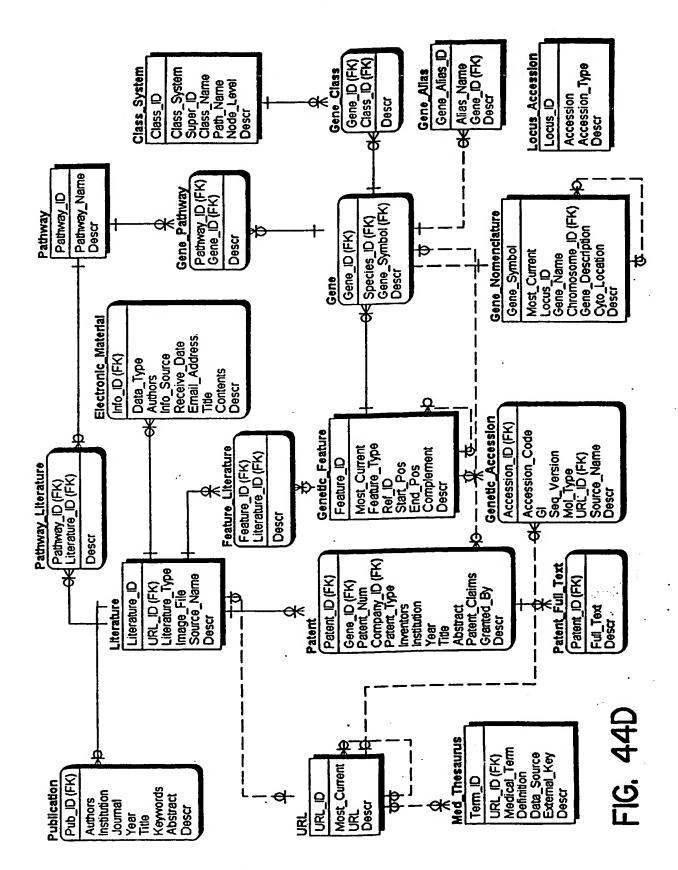
SUBSTITUTE SHEET (RULE 26)



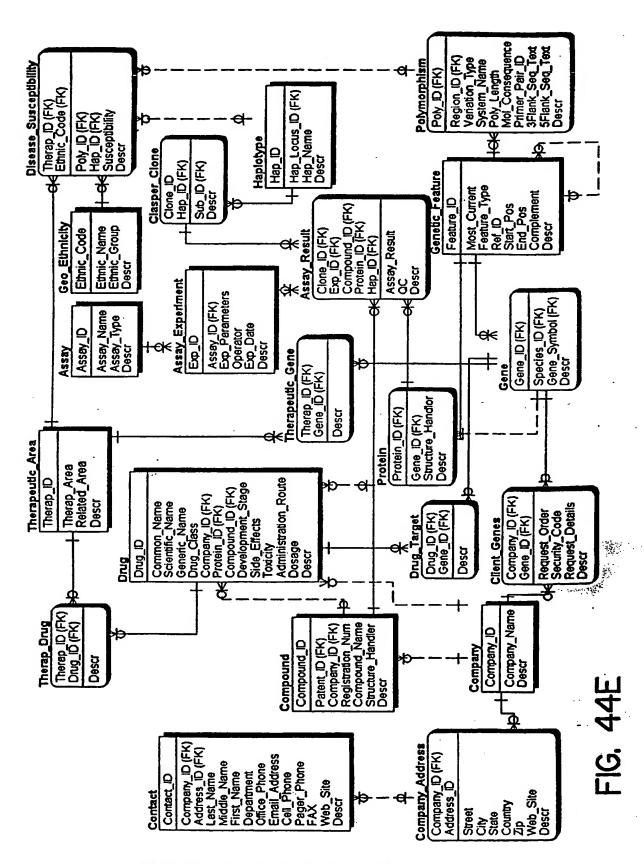
SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)



SUBSTITUTE SHEET (RULE 26)

Legend of Figures:



ample 2

Rectangle Boxes: Tables in the database.

Rounded Boxes: Children tables that depend on their parent tables. This dependency requires that a parent record to be in existence before a child record can be created.

- 2: | Identifying parent / child relationship. It depicts the not nullable 1-to-0-or-many relationship.
- 4: Non-identifying parent / child relationship. It represents the nullable 0-or-1-to-many relationship.
- 6: | Karaman | Identifying parent / child relationship. It depicts the not nullable 1-to-1-or-many relationship.
- 8: +---- Non-identifying parent / child relationship. It represents the not nullable 1-to-1-or-many relationship.
- 10: | Identifying parent / child relationship. It depicts the not nullable 1-to-exact-1 relationship.
- 14: \(\begin{align*}
 \to --- \infty \\
 \text{Non-identifying parent / child relationship. It represents the not nullable 0-or-1-to-many relationship.}\)

FIG. 44F

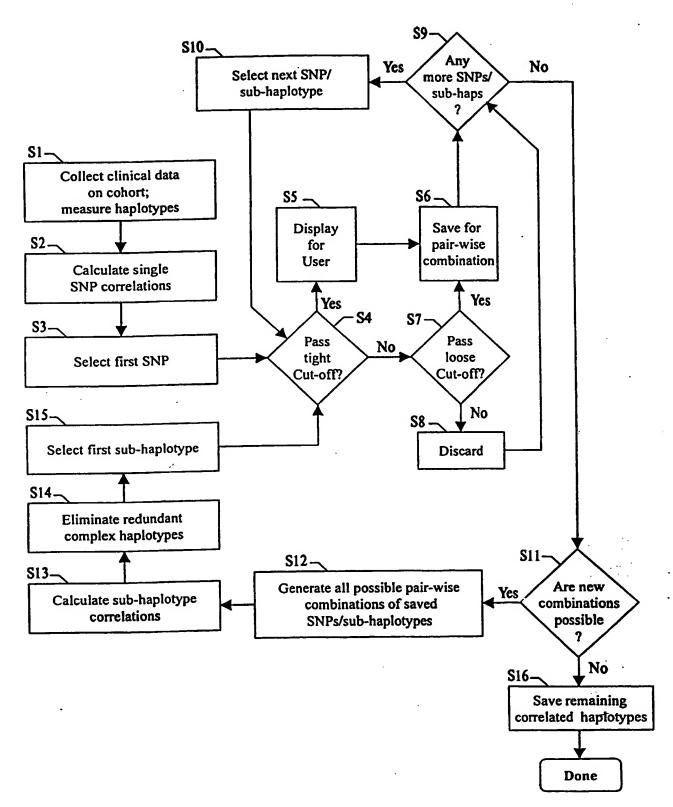


FIG. 45
SUBSTITUTE SHEET (RULE 26)

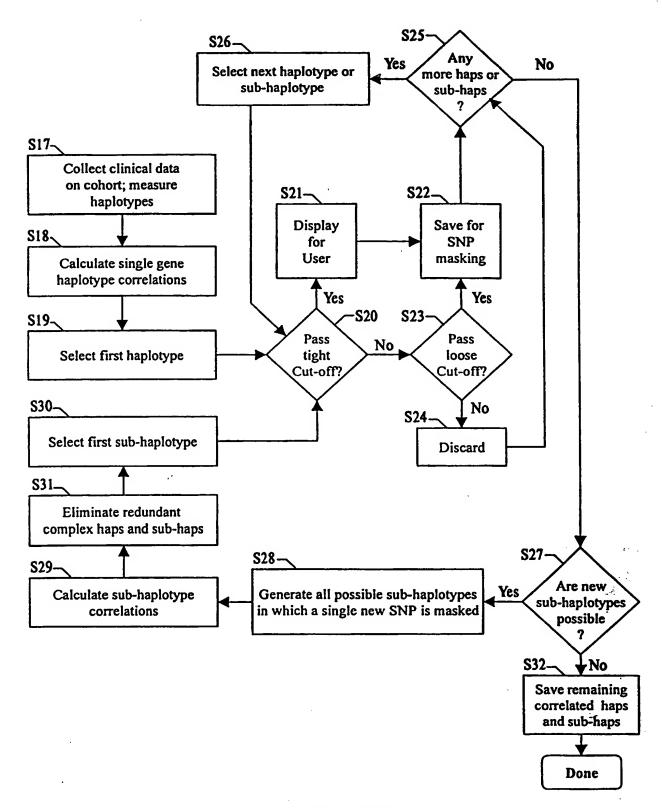


FIG. 46

SUBSTITUTE SHEET (RULE 26)

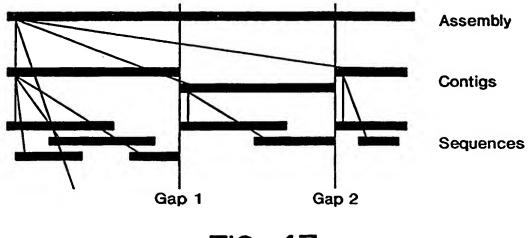


FIG. 47

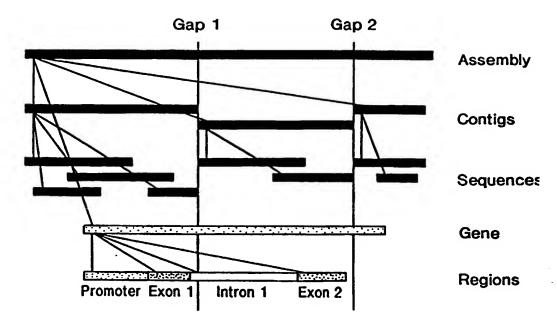


FIG. 48

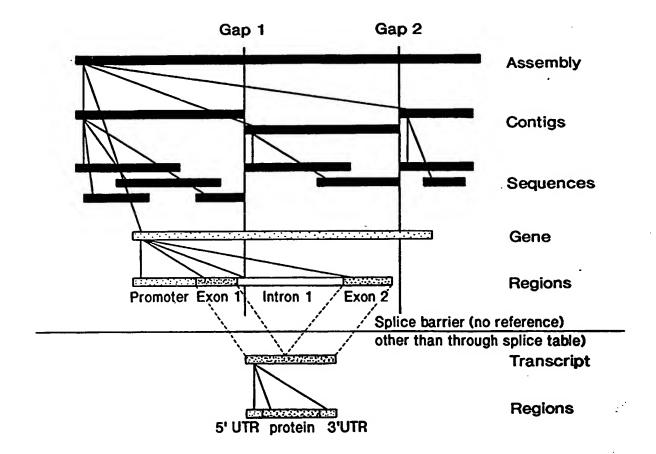


FIG. 49